

**Draft of Revised Claims 11 and 57**  
**U.S. Application No. 09/472,558 to Bahramian et al.**  
**2498/101**

11. (currently amended) A method for muting expression of an endogenous gene in a cultured population of animal cells, the method comprising:

(a) screening to identify~~ying~~ a muting nucleic acid composition having a sequence that is homologous to a sequence in the endogenous gene, the nucleic acid being double stranded ~~[or having the capacity to become double stranded upon delivery to the population of cells]~~, wherein screening to identify~~(ing)~~ comprises the steps of:

(i) designating the entire gene sequence as a potential muting nucleic acid composition;

(ii) identifying a first sequence ~~[muting fragments]~~ of the nucleic acid composition homologous to portions of the endogenous gene that mutes at the level of post-transcription;

(iii) optionally identifying a second sequence that mutes at the level of transcription, wherein both sequences may be part of a single nucleic acid composition;

(b) delivering [the] a muting sequence of the nucleic acid composition into the population of cells; and

(c) muting expression of the endogenous gene ~~[wherein muting comprises muting at the level of post-transcription in the population as a whole, and]~~ wherein such muting is independent of integration[, or expression], ~~or transcription~~ of the delivered nucleic acid.

57. (currently amended) A method for muting expression of an endogenous gene in a cultured population of animal cells, the method comprising:

(a) screening to identify~~[ying]~~ a muting nucleic acid composition having a sequence that is homologous to a sequence in the endogenous gene, wherein the gene is one of a collagen, tumor necrosis factor (TNF), *tat*, and an immunoglobulin gene, the nucleic acid being double stranded ~~[or having the capacity to become double stranded upon delivery to the population of cells]~~, wherein screening to identify~~[ing]~~ comprises the steps of:

(i) designating the entire gene sequence as a potential muting nucleic acid composition;

(ii) identifying a first sequence [muting fragments] of the nucleic acid composition homologous to portions of the endogenous gene that mutes at the level of post-transcription;

(iii) optionally identifying a second sequence that mutes at the level of transcription, wherein both sequences may be part of a single nucleic acid composition;

(b) delivering ~~[the]~~ a muting sequence of the nucleic acid composition into the population of cells; and

(c) muting expression of the endogenous gene ~~[wherein muting comprises muting at the level of post-transcription in the population as a whole, and]~~ wherein such muting is independent of integration[, or expression[, or transcription]] of the delivered nucleic acid.

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